



SEQUENCE LISTING

<110> Blumberg

<120> Methods of Inhibiting Inflammation

<130> 18989-033

<140> 10/808,052

<141> 2004-03-24

<150> 60/457,048

<151> 2003-03-24

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 23

<212> RNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (22)

<223> Wherein n is dT

<220>

<221> misc_feature

<222> (23)

<223> Wherein n is dT

<220>

<223> Description of Artificial Sequence:chemically synthesized siRNA

<400> 1

aagcucugga acuaccaacg ann

23

<210> 2

<211> 23

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chemically synthesized siRNA

<400> 2

ucguugguag uuccagagcu unn

23

<210> 3

<211> 3392

<212> DNA

<213> Homo sapiens

<400> 3

actccctcac tggctgccat taaaagagtc cacttcttag tgactccttag ctgggcactg 60
gatgcagttt aggattgtcg gtcaatatga ttcttcttgc tggctttt ctctgcttca 120
tttcctcata ttcagcttct gttaaaggc acacaactgg tctctcatta aataatgacc 180
ggctgtacaa gctcacgtac tccactgaag ttcttcttgc tcggggcaaa gaaaaactgc 240
aagacagcgt gggctaccgc atttccttca acgtggatgt ggcctacta tggaggaatc 300
ctgatggtga tggatgaccag ttgatccaaa taacgatgaa ggatgtaaat gttgaaaatg 360
tgaatcagca gagaggagag aagagcatct tcaaaggaaa aagccatct aaaataatgg 420
gaaaggaaaa ctttggaaagct ctgcaaaagac ctacgctcct tcacatcaatc catggaaagg 480
tcaaagagtt ctactcatat caaaatgagg cagtggccat agaaaatatc aagagaggc 540
tggcttagcct atttcagaca cagttaaagct ctggaaaccac caatgaggtt gatatctctg 600
gaaattgtaa agtgcacccatc caggctcatc aagacaaaagt gatcaaatt aaggccttgg 660
attcatgcaa aatagcgagg tctggattt cgaccccaaa tcaggtctt ggtgtcagg 720
caaaagctac atctgtcacc acctataaga tagaagacag ctttggattt gctgtctt 780
ctgaagaaaac acacaattttt ggactgaatt tccatccaaa cattaaaggaaa aaaaatgtat 840
cgaagcagaa attagagctg aagacaaccg aagcaggccc aagattgatg tctggaaaagc 900
aggctgcagc cataatcaaa gcagttgattt caaagtttacac ggccatttccc attgtggggc 960
aggtcttcca gagccactgt aaaggatgtc ctctctctc ggagctctgg cggccacca 1020
ggaaatacct gcagcctgac aaccttcca aggctgaggc tgtcagaaac tccctggct 1080
tcattcagca cctcaggact gcaaggaaaag aagagatcct tcaaatacta aagatggaaa 1140
ataaggaagt attacctcg ctgggtggat tttggatttca aagatgacag cagcattatc ctccaggaga 1200
tagaagccat tttggacttt ttggatttca aagatgacag cagcattatc ctccaggaga 1260
ggtttctcta tgcctgtgga tttgcttctc atcccaatga agaactcctg agagccctca 1320
tttagtaagtt caaagggttctt atggtagca gtgacatcag agaaaactgtt atgatcatca 1380
ctgggacact tgcagaaaag ttgtgtcaga atgaaggctg caaaactcaaa gcagtagtgg 1440
aagctaagaa gttaatcctg ggaggacttgg aaaaaggcaga gaaaaaaagag gacaccagga 1500
tgtatctgct ggctttaaggg aatgccctgc ttccagaagg catcccaagt ttctgtaaat 1560
atgcagaagc aggagaaggg cccatcagcc acctggctac cactgctctc cagagatatg 1620
atctccctt cataactgtat gaggtgaaga agaccttaaa cagaatatac caccaaaaacc 1680
gtaaagttca tggaaaagact gtgcgcactg ctgcagctgc tatcatttt aataacaatc 1740
catcctacat ggacgtcaag aacatcctgc tgcattttgg ggagcttccc caagaaatga 1800
ataaatacat gctgccattt ttgtccgtcg agttctgaag gaaatggctg ctcacaatattt tgaccgtttc tccaggagtg 1860
gatcttcttc tgcttactact ggctacatag aacgttagtcc ccgttccggca tctacttaca 1920
gccttagacat tcttactcg gttctggca ttctaaaggag aagtaacctg aacatcttc 2040
agtacattgg gaaggctggc cttcacggta gccagggtgg tattgaagcc caaggactgg 2100
aaggcttaat cgccagccacc cctgacgagg gggaggagaa ccttgaactcc tatgctggta 2160
tgtcagccat cctttttgtat gttcagctca gacctgtcactt cttttcaac ggatacagtg 2220
atttgatgtc caaaaatgtcg tcagcatctg gcgaccctat cagtgtggt aaaggactta 2280
ttctgctaat agatcattct caggaacttc atttacaatc tggactaaaa gccaatatac 2340
aggtccaggg tggcttagct atttgatattt caggtgcaat ggagtttagc ttgtggatc 2400
gtgagttcaa aacccgagtg aaaaataggg tgactgtggt aataaccact gacatcacag 2460
tggactccctc ttttggaaa gctggctgg aaaccagttac agaaaacagaa gcaggcttgg 2520
agtttatctc cacagtgcag ttttctcactt acccatttctt agtttgcattt cagatggaca 2580
aggatgaagc tccattcagg caatttggaa aaaaatgtacga aaggctgtcc acaggcagag 2640
gttatgtctc tcagaaaaaaa aaaaatgtacgaa tatttagcagg atgtgaattt cccgtccatc 2700
aagagaactc agagatgtgc aaagtgggtt ttggccctca gccggatagt acttccagcg 2760
gtgggtttt gaaactgaccc tggatattttt acttgaattt gtctccccga aaggggacaca 2820
atgtggcatg actaagtact tgctcttgc gacccacagcg tttacatatt tacctgtatt 2880
taagattttt gtaaaaaagct aaaaaaaaaact gcagtttgcattt caaatggg tatatgcagt 2940
atgctaccca cagcgtcattt tggatcatc atgtgacgc ttcacaaacg ttcttagttt 3000
acttataacct ctctccaaatc tcatttggta cagtcagaat agttattctc taagagggaaa 3060
ctagtgtttt taaaaaacaatc aaaaatggaaa aaaaaccacac aaggagaacc caatgggtt 3120
tcaacaatccat tggatcaatg tttatgtacgc ttttgcattt gcatgacggg 3180
aaaaccaaaac acgttccctt aatggggaaa aaaaatgtaa gacacaaaaca 3240

aaccattttt ttctctttt ttggagttgg gggcccaggg agaagggaca aggctttaa 3300
aagactgtt agccaacttc aagaattaat atttatgtct ctgttattgt tagtttaag 3360
ccttaaggta gaaggcacat agaaataaca tc 3392

<210> 4
<211> 894
<212> PRT
<213> Homo sapiens

<400> 4
Met Ile Leu Leu Ala Val Leu Phe Leu Cys Phe Ile Ser Ser Tyr Ser
1 5 10 15
Ala Ser Val Lys Gly His Thr Thr Gly Leu Ser Leu Asn Asn Asp Arg
20 25 30
Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Leu Leu Asp Arg Gly Lys
35 40 45
Gly Lys Leu Gln Asp Ser Val Gly Tyr Arg Ile Ser Ser Asn Val Asp
50 55 60
Val Ala Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Asp Gln Leu Ile
65 70 75 80
Gln Ile Thr Met Lys Asp Val Asn Val Glu Asn Val Asn Gln Gln Arg
85 90 95
Gly Glu Lys Ser Ile Phe Lys Gly Lys Ser Pro Ser Lys Ile Met Gly
100 105 110
Lys Glu Asn Leu Glu Ala Leu Gln Arg Pro Thr Leu Leu His Leu Ile
115 120 125
His Gly Lys Val Lys Glu Phe Tyr Ser Tyr Gln Asn Glu Ala Val Ala
130 135 140
Ile Glu Asn Ile Lys Arg Gly Leu Ala Ser Leu Phe Gln Thr Gln Leu
145 150 155 160
Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asn Cys Lys Val
165 170 175
Thr Tyr Gln Ala His Gln Asp Lys Val Ile Lys Ile Lys Ala Leu Asp
180 185 190
Ser Cys Lys Ile Ala Arg Ser Gly Phe Thr Thr Pro Asn Gln Val Leu
195 200 205
Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp
210 215 220
Ser Phe Val Ile Ala Val Leu Ala Glu Glu Thr His Asn Phe Gly Leu
225 230 235 240
Asn Phe Leu Gln Thr Ile Lys Gly Lys Ile Val Ser Lys Gln Lys Leu

245	250	255	
Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Leu Met Ser Gly Lys Gln			
260	265	270	
Ala Ala Ala Ile Ile Lys Ala Val Asp Ser Lys Tyr Thr Ala Ile Pro			
275	280	285	
Ile Val Gly Gln Val Phe Gln Ser His Cys Lys Gly Cys Pro Ser Leu			
290	295	300	
Ser Glu Leu Trp Arg Ser Thr Arg Lys Tyr Leu Gln Pro Asp Asn Leu			
305	310	315	320
Ser Lys Ala Glu Ala Val Arg Asn Phe Leu Ala Phe Ile Gln His Leu			
325	330	335	
Arg Thr Ala Lys Lys Glu Glu Ile Leu Gln Ile Leu Lys Met Glu Asn			
340	345	350	
Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr			
355	360	365	
Ser Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp			
370	375	380	
Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala			
385	390	395	400
Ser His Pro Asn Glu Glu Leu Leu Arg Ala Leu Ile Ser Lys Phe Lys			
405	410	415	
Gly Ser Ile Gly Ser Ser Asp Ile Arg Glu Thr Val Met Ile Ile Thr			
420	425	430	
Gly Thr Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys			
435	440	445	
Ala Val Val Glu Ala Lys Lys Leu Ile Leu Gly Gly Leu Glu Lys Ala			
450	455	460	
Glu Lys Lys Glu Asp Thr Arg Met Tyr Leu Leu Ala Leu Lys Asn Ala			
465	470	475	480
Leu Leu Pro Glu Gly Ile Pro Ser Leu Leu Lys Tyr Ala Glu Ala Gly			
485	490	495	
Glu Gly Pro Ile Ser His Leu Ala Thr Thr Ala Leu Gln Arg Tyr Asp			
500	505	510	
Leu Pro Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr			
515	520	525	
His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Ala Ala Ala			
530	535	540	
Ala Ile Ile Leu Asn Asn Pro Ser Tyr Met Asp Val Lys Asn Ile			

545	550	555	560
Leu Leu Ser Ile Gly Glu Leu Pro Gln Glu Met Asn Lys Tyr Met Leu			
565	570	575	
Ala Ile Val Gln Asp Ile Leu Arg Leu Glu Met Pro Ala Ser Lys Ile			
580	585	590	
Val Arg Arg Val Leu Lys Glu Met Val Ala His Asn Tyr Asp Arg Phe			
595	600	605	
Ser Arg Ser Gly Ser Ser Ala Tyr Thr Gly Tyr Ile Glu Arg Ser			
610	615	620	
Pro Arg Ser Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser			
625	630	635	640
Gly Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Gly Lys			
645	650	655	
Ala Gly Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu			
660	665	670	
Ala Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser			
675	680	685	
Tyr Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val			
690	695	700	
Thr Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala			
705	710	715	720
Ser Gly Asp Pro Ile Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp			
725	730	735	
His Ser Gln Glu Leu Gln Leu Gln Ser Gly Leu Lys Ala Asn Ile Glu			
740	745	750	
Val Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ala Met Glu Phe Ser			
755	760	765	
Leu Trp Tyr Arg Glu Ser Lys Thr Arg Val Lys Asn Arg Val Thr Val			
770	775	780	
Val Ile Thr Thr Asp Ile Thr Val Asp Ser Ser Phe Val Lys Ala Gly			
785	790	795	800
Leu Glu Thr Ser Thr Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr			
805	810	815	
Val Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys			
820	825	830	
Asp Glu Ala Pro Phe Arg Gln Phe Glu Lys Lys Tyr Glu Arg Leu Ser			
835	840	845	
Thr Gly Arg Gly Tyr Val Ser Gln Lys Arg Lys Glu Ser Val Leu Ala			

850

855

860

Gly Cys Glu Phe Pro Leu His Gln Glu Asn Ser Glu Met Cys Lys Val
 865 870 875 880

Val Phe Ala Pro Gln Pro Asp Ser Thr Ser Ser Gly Trp Phe
 885 890

<210> 5
 <211> 2878
 <212> DNA
 <213> Mus musculus

<400> 5

ctggatgtgg cagagggagc cagcatgatc ctcttggcag tgcttttct ctgcttc 60
 tcctcctact ctgcttcgt taaaggtcac acaactggcc tctcattaaa taatgagcgg 120
 ctatacaagc tcacgtactc cactgaagt tttcttgcgt ggggcaaagg aaaaccgcaa 180
 gacagcgtgg gctacaaaat ctcatctgtat gtggacgtt gttactgtg gaggaatcct 240
 gatggtgatg atgatcaagt gatccaagt acgataacag ctgttaacgt tgaaaatgct 300
 ggtcaacaga gaggcgagaa gaggatctc cagggcaaaa gtacacctaa gatcataggg 360
 aaggacaacc tggaggctct gcagagaccc atgcttc 420
 aaggagttct actcctatga aaacgagcca gtgggcatag aaaatctcaa gagaggctt 480
 gctagcttat tccagatgca gctaaagctt ggaactacca acgaggttata tatctctggg 540
 gattgtaaag tgacctacca ggcccaacaa gacaaagtgg tcaaaattaa ggctctggat 600
 acatgcaaaa ttgagcgtc tggatttaca acggcaacc aggtgctggg cgtcagttca 660
 aaagccacat ctgtcaactac ctacaagata gaggacagct ttgtcaccgc tgcgttgc 720
 gaagagacca gggctttgc cttgaacttca caacaaacca tagcaggaaa aatagtgtca 780
 aagcagaaat tggagctgaa gacaactgaa gccggcccaa ggtatgtccc cgggaagcaa 840
 gtggcaggtg taattaaagc agttgattcc aaatacacaag ccattcccat tggggacag 900
 gtcctcgagc gtgtctgcaa aggatgccct tctctggcg aggactggaa gtccatcaga 960
 aagaacctgg agcctgaaaaa cctgtccaaag gcccggctg tccagagctt cctggccttc 1020
 atccagcacc tccggacttca gaggagagaa gagatcttcc agattctgaa ggcagagaag 1080
 aaagaagtgc tccctcagct ggtggatgcc gtcacccctg ctcagactcc agactcgcta 1140
 gaagccatcc tggactttt ggatttcaaa agtgcacgca gtatcatact ccaggaaagg 1200
 ttccctctatg cctgtggctt tgccacccac cctgtatgaa aactcctacg agccctcctt 1260
 agtaagttca aagggttccct tgcaagcaac gacatcagag agtcggat tgcattcatt 1320
 ggagccctag tcaggaagct gtgtcagaat gaaggctgca agctcaaggc agtggtgaa 1380
 gctaagaagc tgatcctgg aggacttcaa aaaccagaga agaaaagaaga caccacaatg 1440
 tacctgctgg ccctgaagaa tgccttgctt cccgaaggca tcccgctcct tctgaagtat 1500
 gctgaggctg gagaaggcc cgtcagccac ctggccacca ctgttctcca gagatacgat 1560
 gtctccctca tcacagatga ggtgaagaag accttgaaca ggatatacca ccagaatcgt 1620
 aaggttcatg agaagacggt ggcacaaact gcccgtctg tcatacttaaa gaaccatcc 1680
 tacatggatg tgaagaacat cctgtgtcc attggggaaac tcccgaaaga gatgaacaaa 1740
 tacatgctca ccgttgtca agacatcctg cattttgaaa tgcctgcaag caaatgatc 1800
 cgtcgagttc tcaaggagat ggctgttccac aattatgacc gtttctccaa gagtggatcc 1860
 tcttcgttca atactggcta cgtagaacgt agccccctg cagcgtccac atacagcctt 1920
 gacatccctt actctggctc tggcattctg aggagaagta acctgaacat cttccagtac 1980
 atcaaaggaa cagagctca tggtagtca gttgtgattt aagcccaagg gctggaaaggc 2040
 ttaattgcag ccactccatg tgaaggagag gagaacctt gactcttatgc tggcatgtca 2100
 gccatccctgt ttgatgttca gcttaggcct gtcacat ttaatggata cagtgattt 2160
 atgtccaaaa tgcgtgtccgc atccggcgcac cctgtcagcg tggtaaagg gcttattctg 2220
 ttaatagacc attctcagga tattcagctg caatctggac taaaggccaa tatggagatc 2280
 cagggtggtc tagctattga tatttctgg tcaatggaaat tcagtctgtg gtatcgccg 2340
 tctaaaaccc gagtgaaaaa tcgggtggct gtggtgataa ccagcgacgt cacagtggat 2400
 gccttttttgc taaaagctgg tctggaaaggc agagcggaga cagaggctgg gctggagttc 2460
 atctccacag tgcagttctc acagtaccgc ttcttggctt gcatgcagat ggacaaggct 2520

gaaggccccac tcaggcaatt cgagacaaag tatgaaaggc tatctacagg cagggatat 2580
gtctctcgga gaagaaaaga gagcctagtg gccggatgtg aactccccct ccatcaacag 2640
aactctgaga tgtgcaacgt ggtattccca cctcagccag aaagcgataa ctccggtgga 2700
tggtttgat tcccgtgggt tcccttccac cagaacgata tgctatgacg tgccctgaccc 2760
ttgctctctg agagcacagt gttacatat ttacctgtat ttaagatgtt tgtaaagagc 2820
agtggagaac ttcagttgat taaagttgaa cctattcagg agaagaccca cagtgtcc 2878

<210> 6
<211> 894
<212> PRT
<213> Mus musculus

<400> 6
Met Ile Leu Leu Ala Val Leu Phe Leu Cys Phe Phe Ser Ser Tyr Ser
1 5 10 15
Ala Ser Val Lys Gly His Thr Thr Gly Leu Ser Leu Asn Asn Glu Arg
20 25 30
Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Phe Leu Asp Gly Gly Lys
35 40 45
Gly Lys Pro Gln Asp Ser Val Gly Tyr Lys Ile Ser Ser Asp Val Asp
50 55 60
Val Val Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Asp Gln Val Ile
65 70 75 80
Gln Val Thr Ile Thr Ala Val Asn Val Glu Asn Ala Gly Gln Gln Arg
85 90 95
Gly Glu Lys Ser Ile Phe Gln Gly Lys Ser Thr Pro Lys Ile Ile Gly
100 105 110
Lys Asp Asn Leu Glu Ala Leu Gln Arg Pro Met Leu Leu His Leu Val
115 120 125
Arg Gly Lys Val Lys Glu Phe Tyr Ser Tyr Glu Asn Glu Pro Val Gly
130 135 140
Ile Glu Asn Leu Lys Arg Gly Leu Ala Ser Leu Phe Gln Met Gln Leu
145 150 155 160
Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asp Cys Lys Val
165 170 175
Thr Tyr Gln Ala Gln Gln Asp Lys Val Val Lys Ile Lys Ala Leu Asp
180 185 190
Thr Cys Lys Ile Glu Arg Ser Gly Phe Thr Thr Ala Asn Gln Val Leu
195 200 205
Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp
210 215 220
Ser Phe Val Thr Ala Val Leu Ala Glu Glu Thr Arg Ala Phe Ala Leu

225	230	235	240
Asn Phe Gln Gln Thr Ile Ala Gly Lys Ile Val Ser Lys Gln Lys Leu			
245	250	255	
Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Met Ile Pro Gly Lys Gln			
260	265	270	
Val Ala Gly Val Ile Lys Ala Val Asp Ser Lys Tyr Lys Ala Ile Pro			
275	280	285	
Ile Val Gly Gln Val Leu Glu Arg Val Cys Lys Gly Cys Pro Ser Leu			
290	295	300	
Ala Glu His Trp Lys Ser Ile Arg Lys Asn Leu Glu Pro Glu Asn Leu			
305	310	315	320
Ser Lys Ala Glu Ala Val Gln Ser Phe Leu Ala Phe Ile Gln His Leu			
325	330	335	
Arg Thr Ser Arg Arg Glu Glu Ile Leu Gln Ile Leu Lys Ala Glu Lys			
340	345	350	
Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr			
355	360	365	
Pro Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp			
370	375	380	
Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala			
385	390	395	400
Thr His Pro Asp Glu Glu Leu Leu Arg Ala Leu Leu Ser Lys Phe Lys			
405	410	415	
Gly Ser Phe Ala Ser Asn Asp Ile Arg Glu Ser Val Met Ile Ile Ile			
420	425	430	
Gly Ala Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys			
435	440	445	
Ala Val Val Glu Ala Lys Leu Ile Leu Gly Gly Leu Glu Lys Pro			
450	455	460	
Glu Lys Lys Glu Asp Thr Thr Met Tyr Leu Leu Ala Leu Lys Asn Ala			
465	470	475	480
Leu Leu Pro Glu Gly Ile Pro Leu Leu Leu Lys Tyr Ala Glu Ala Gly			
485	490	495	
Glu Gly Pro Val Ser His Leu Ala Thr Thr Val Leu Gln Arg Tyr Asp			
500	505	510	
Val Ser Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr			
515	520	525	
His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Thr Ala Ala			

530

535

540

Ala Val Ile Leu Lys Asn Pro Ser Tyr Met Asp Val Lys Asn Ile Leu
 545 550 555 560

Leu Ser Ile Gly Glu Leu Pro Lys Glu Met Asn Lys Tyr Met Leu Thr
 565 570 575

Val Val Gln Asp Ile Leu His Phe Glu Met Pro Ala Ser Lys Met Ile
 580 585 590

Arg Arg Val Leu Lys Glu Met Ala Val His Asn Tyr Asp Arg Phe Ser
 595 600 605

Lys Ser Gly Ser Ser Ser Ala Tyr Thr Gly Tyr Val Glu Arg Ser Pro
 610 615 620

Arg Ala Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser Gly
 625 630 635 640

Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Lys Gly Thr
 645 650 655

Glu Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu Gly
 660 665 670

Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser Tyr
 675 680 685

Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val Thr
 690 695 700

Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala Ser
 705 710 715 720

Gly Asp Pro Val Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp His
 725 730 735

Ser Gln Asp Ile Gln Leu Gln Ser Gly Leu Lys Ala Asn Met Glu Ile
 740 745 750

Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ser Met Glu Phe Ser Leu
 755 760 765

Trp Tyr Arg Glu Ser Lys Thr Arg Val Lys Asn Arg Val Ala Val Val
 770 775 780

Ile Thr Ser Asp Val Thr Val Asp Ala Ser Phe Val Lys Ala Gly Leu
 785 790 795 800

Glu Ser Arg Ala Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr Val
 805 810 815

Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys Ala
 820 825 830

Glu Ala Pro Leu Arg Gln Phe Glu Thr Lys Tyr Glu Arg Leu Ser Thr

835	840	845
Gly Arg Gly Tyr Val Ser Arg Arg Arg Lys Glu Ser Leu Val Ala Gly		
850	855	860
Cys Glu Leu Pro Leu His Gln Gln Asn Ser Glu Met Cys Asn Val Val		
865	870	875
Phe Pro Pro Gln Pro Glu Ser Asp Asn Ser Gly Gly Trp Phe		
885	890	

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide primer

<400> 7
 ggagaaaacgg tcataattgt g 21

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide primer

<400> 8
 gtggggccgct ctaggcacca a 21

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide primer

<400> 9
 ctctttgatg tcacgcacga tttc 24

<210> 10
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence:oligonucleotide primer

<400> 10
ggactttttg gatttcaaaa gtgac

25

<210> 11
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(261)
<223> Wherein Xaa is any amino acid.

<400> 11
Met Asp Pro Pro Arg Pro Ala Leu Leu Ala Leu Leu Ala Xaa Pro Xaa
1 5 10 15

Leu Leu Leu Leu Leu Ala Gly Ala Arg Xaa Glu Glu Glu Xaa Leu
20 25 30

Glu Asn Val Xaa Leu Val Cys Pro Lys Asp Xaa Thr Arg Phe Xaa His
35 40 45

Leu Xaa Lys Xaa Xaa Thr Tyr Asn Tyr Glu Ala Glu Ser Ser Ser Gly
50 55 60

Val Pro Gly Thr Ala Xaa Ser Arg Ser Ala Thr Arg Xaa Asn Cys Lys
65 70 75 80

Xaa Glu Leu Glu Val Pro Gln Leu Cys Ser Phe Ile Leu Lys Xaa Ser
85 90 95

Gln Cys Thr Leu Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys Ala
100 105 110

Leu Leu Lys Lys Thr Lys Asn Ser Xaa Glu Xaa Ala Ala Ala Met Ser
115 120 125

Arg Xaa Glu Leu Lys Leu Ala Ile Pro Glu Gly Lys Gln Val Phe Leu
130 135 140

Tyr Pro Glu Lys Asp Glu Pro Thr Tyr Ile Leu Asn Ile Lys Arg Gly
145 150 155 160

Ile Ile Ser Ala Leu Leu Val Pro Pro Glu Xaa Glu Glu Ala Lys Gln
165 170 175

Xaa Leu Phe Xaa Asp Thr Val Tyr Gly Asn Cys Ser Thr His Phe Thr
180 185 190

Val Lys Thr Arg Xaa Gly Asn Xaa Ala Thr Xaa Xaa Ser Thr Glu Arg
195 200 205

Asp Leu Gly Gln Cys Asp Arg Phe Lys Pro Ile Arg Thr Gly Ile Ser
210 215 220

Pro Xaa Ala Leu Ile Lys Gly Met Xaa Arg Pro Leu Ser Thr Leu Ile
225 230 235 240

Xaa Ser Xaa Gln Ser Cys Gln Xaa Thr Leu Asp Ala Lys Arg Lys His
245 250 255

Val Ala Glu Ala Xaa Cys Lys Glu Gln
260 265

<210> 12

<211> 335

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)..(335)

<223> Wherein Xaa is any amino acid.

<400> 12

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
35 40 45

Trp Leu Gly Glu Leu Gln Thr His Xaa Trp Ser Asn Asp Ser Asp Thr
50 55 60

Val Arg Xaa Xaa Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
65 70 75 80

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
85 90 95

Xaa Asp Xaa Lys Glu Xaa Ala Lys Xaa Xaa Arg Leu Ser Tyr Pro Leu
100 105 110

Glu Leu Gln Xaa Ser Ala Gly Cys Glu Xaa His Pro Gly Asn Ala Ser
115 120 125

Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
130 135 140

Gln Gly Thr Ser Xaa Glu Pro Xaa Gln Glu Ala Pro Xaa Trp Val Asn
145 150 155 160

Leu Ala Xaa Gln Xaa Leu Asn Gln Asp Lys Trp Thr Xaa Glu Thr Xaa
165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
 180 185 190
 Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Xaa Trp
 195 200 205
 Leu Ser Arg Gly Pro Xaa Pro Xaa Pro Gly Arg Leu Leu Leu Xaa Cys
 210 215 220
 His Val Ser Gly Xaa Tyr Pro Lys Pro Val Trp Val Lys Trp Xaa Xaa
 225 230 235 240
 Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Xaa Asp Xaa Xaa Pro Asn
 245 250 255
 Xaa Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Xaa Val Xaa Ala Gly
 260 265 270
 Glu Ala Xaa Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Xaa Gly
 275 280 285
 Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
 290 295 300
 Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
 305 310 315 320
 Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
 325 330 335

<210> 13
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(210)
 <223> Wherein Xaa is any amino acid.

<400> 13
 Lys Cys Val Gln Ser Xaa Lys Pro Ser Leu Met Ile Gln Lys Ala Xaa
 1 5 10 15
 Xaa Gln Ala Leu Arg Lys Met Glu Pro Lys Asp Lys Asp Gln Glu Val
 20 25 30
 Leu Leu Gln Thr Phe Leu Asp Asp Ala Ser Pro Gly Asp Xaa Arg Xaa
 35 40 45
 Ala Ala Xaa Leu Met Xaa Xaa Arg Ser Pro Ser Gln Ala Asp Xaa Asn
 50 55 60
 Lys Ile Val Gln Xaa Leu Pro Trp Glu Gln Asn Glu Gln Val Lys Asn
 65 70 75 80

Xaa Val Ala Xaa His Ile Ala Asn Xaa Leu Asn Ser Glu Glu Xaa Asp
85 90 95

Xaa Gln Asp Leu Lys Lys Leu Val Xaa Glu Ala Xaa Lys Glu Ser Gln
100 105 110

Leu Pro Thr Val Met Asp Phe Arg Lys Phe Ser Arg Asn Tyr Gln Leu
115 120 125

Tyr Lys Ser Val Xaa Leu Pro Ser Leu Asp Pro Xaa Ser Xaa Lys Ile
130 135 140

Glu Gly Asn Leu Xaa Phe Asp Pro Asn Asn Xaa Leu Pro Lys Glu Ser
145 150 155 160

Met Xaa Xaa Thr Thr Leu Thr Ala Phe Gly Phe Ala Ser Xaa Asp Xaa
165 170 175

Xaa Glu Ile Xaa Leu Glu Gly Lys Gly Phe Glu Pro Thr Leu Xaa Ala
180 185 190

Xaa Phe Gly Lys Gln Xaa Phe Phe Pro Xaa Ser Val Asn Lys Ala Leu
195 200 205

Tyr Trp
210

<210> 14
<211> 301
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)..(301)
<223> Wherein Xaa is any amino acid.

<400> 14
Phe Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val Thr Gln Thr
1 5 10 15

Leu Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe Phe Gly Glu
20 25 30

Gly Thr Xaa Lys Met Gly Leu Ala Xaa Glu Ser Thr Lys Ser Thr Ser
35 40 45

Pro Pro Lys Xaa Ala Glu Ala Val Xaa Xaa Xaa Leu Gln Glu Leu Lys
50 55 60

Lys Leu Thr Ile Ser Xaa Gln Xaa Ile Gln Arg Ala Xaa Leu Phe Asn
65 70 75 80

Xaa Xaa Val Thr Glu Leu Arg Gly Leu Ser Asp Glu Ala Val Thr Ser
85 90 95

Xaa Leu Pro Gln Leu Ile Glu Xaa Ser Ser Pro Xaa Xaa Leu Gln Ala
 100 105 110
 Leu Val Gln Cys Gly Xaa Pro Gln Cys Ser Thr His Ile Xaa Gln Xaa
 115 120 125
 Leu Lys Xaa Val His Ala Asn Pro Leu Leu Ile Asp Val Val Thr Tyr
 130 135 140
 Leu Val Ala Leu Xaa Pro Glu Pro Ser Ala Gln Gln Xaa Arg Glu Ile
 145 150 155 160
 Phe Asn Met Ala Arg Xaa Gln Arg Ser Arg Ala Thr Leu Tyr Ala Leu
 165 170 175
 Ser His Ala Val Asn Asn Tyr His Lys Xaa Asn Pro Xaa Gly Thr Gln
 180 185 190
 Glu Leu Xaa Asp Ile Ala Asn Xaa Leu Met Glu Gln Ile Gln Asp Asp
 195 200 205
 Cys Xaa Gly Asp Glu Asp Tyr Thr Tyr Leu Xaa Leu Arg Xaa Ile Gly
 210 215 220
 Asn Met Gly Gln Thr Met Glu Gln Leu Thr Pro Glu Leu Lys Ser Xaa
 225 230 235 240
 Ile Leu Lys Cys Val Gln Ser Thr Lys Pro Ser Xaa Xaa Ile Gln Lys
 245 250 255
 Ala Ala Ile Gln Xaa Leu Arg Lys Met Glu Pro Lys Asp Lys Asp Gln
 260 265 270
 Xaa Xaa Leu Leu Gln Thr Phe Leu Asp Asp Ala Ser Pro Gly Asp Lys
 275 280 285
 Arg Leu Ala Ala Tyr Leu Met Leu Xaa Arg Ser Pro Ser
 290 295 300

<210> 15
 <211> 335
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(335)
 <223> Wherein Xaa is any amino acid.

<400> 15
 Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
 1 5 10 15
 Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
 20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
 35 40 45

Trp Leu Gly Glu Leu Gln Thr His Xaa Trp Ser Asn Asp Ser Asp Thr
 50 55 60

Val Arg Xaa Xaa Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
 65 70 75 80

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
 85 90 95

Xaa Asp Xaa Lys Glu Xaa Ala Lys Xaa Xaa Arg Leu Ser Tyr Pro Leu
 100 105 110

Glu Leu Gln Xaa Ser Ala Gly Cys Glu Xaa His Pro Gly Asn Ala Ser
 115 120 125

Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
 130 135 140

Gln Gly Thr Ser Xaa Glu Pro Xaa Gln Glu Ala Pro Xaa Trp Val Asn
 145 150 155 160

Leu Ala Xaa Gln Xaa Leu Asn Gln Asp Lys Trp Thr Xaa Glu Thr Xaa
 165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
 180 185 190

Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Xaa Trp
 195 200 205

Leu Ser Arg Gly Pro Xaa Pro Xaa Pro Gly Arg Leu Leu Leu Xaa Cys
 210 215 220

His Val Ser Gly Xaa Tyr Pro Lys Pro Val Trp Val Lys Trp Xaa Xaa
 225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Xaa Asp Xaa Xaa Pro Asn
 245 250 255

Xaa Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Xaa Val Xaa Ala Gly
 260 265 270

Glu Ala Xaa Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Xaa Gly
 275 280 285

Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
 290 295 300

Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
 305 310 315 320

Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
 325 330 335

<210> 16
<211> 335
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)..(335)
<223> Wherein Xaa is any amino acid.

<400> 16
Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Xaa Thr Asp Gly Leu Ala
35 40 45

Xaa Leu Gly Glu Leu Gln Thr His Ser Trp Ser Xaa Asp Ser Asp Thr
50 55 60

Xaa Xaa Xaa Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Xaa Gln Xaa
65 70 75 80

Trp Glu Thr Leu Xaa His Ile Phe Xaa Xaa Tyr Arg Ser Ser Phe Thr
85 90 95

Arg Asp Val Lys Glu Phe Ala Lys Xaa Leu Arg Leu Ser Tyr Pro Xaa
100 105 110

Glu Leu Gln Xaa Xaa Ala Gly Cys Glu Val His Pro Gly Xaa Ala Ser
115 120 125

Asn Asn Phe Phe His Xaa Ala Xaa Gln Gly Xaa Asp Ile Leu Ser Phe
130 135 140

Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Xaa Trp Val Asn
145 150 155 160

Leu Ala Ile Gln Xaa Leu Asn Gln Asp Lys Trp Thr Arg Xaa Thr Val
165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
180 185 190

Glu Xaa Gly Lys Xaa Glu Leu Lys Lys Gln Xaa Lys Pro Lys Ala Xaa
195 200 205

Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
210 215 220

His Val Xaa Gly Phe Tyr Pro Lys Pro Val Trp Xaa Lys Trp Xaa Arg
225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
245 250 255

Xaa Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Xaa Xaa Ala Gly
260 265 270

Glu Ala Ala Gly Leu Xaa Cys Arg Val Lys His Ser Ser Leu Glu Gly
275 280 285

Gln Xaa Xaa Xaa Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
290 295 300

Ile Ala Leu Ala Val Leu Ala Cys Leu Xaa Phe Leu Leu Ile Val Gly
305 310 315 320

Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
325 330 335